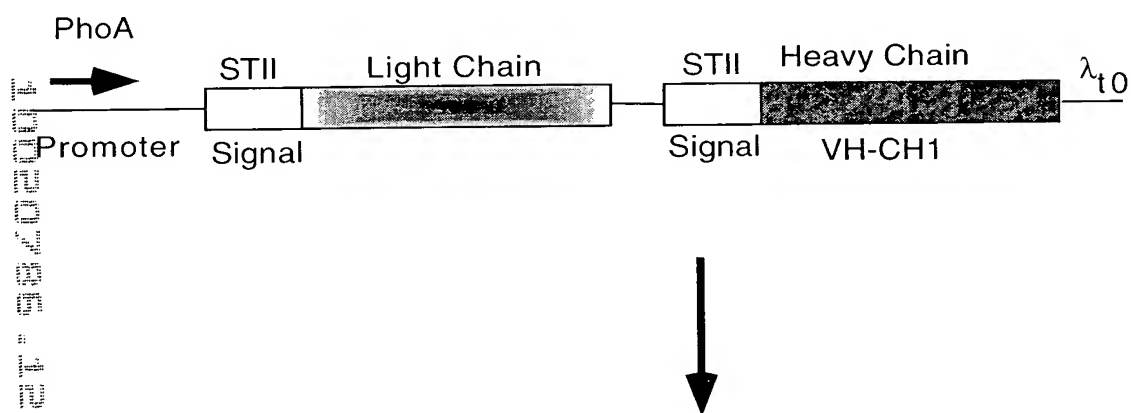


Fab Expression Vector pAK19



Full Length Antibody Expression Vector Derived from pAK19

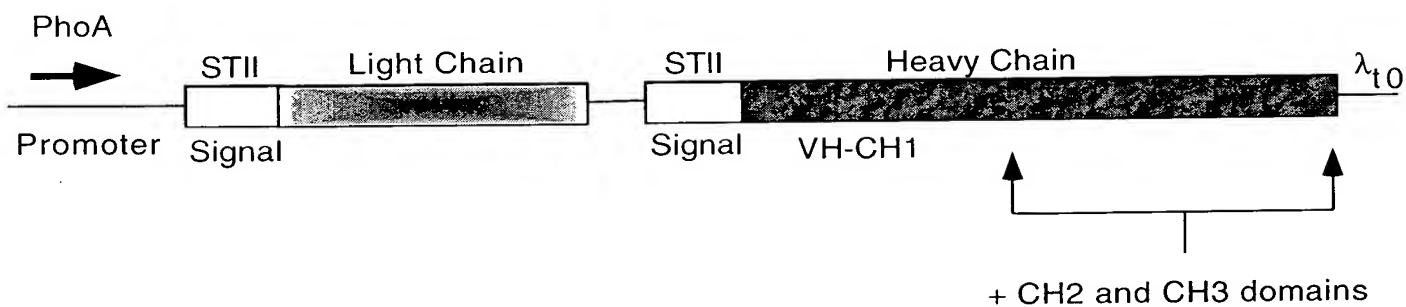


Figure 1

100098-1394

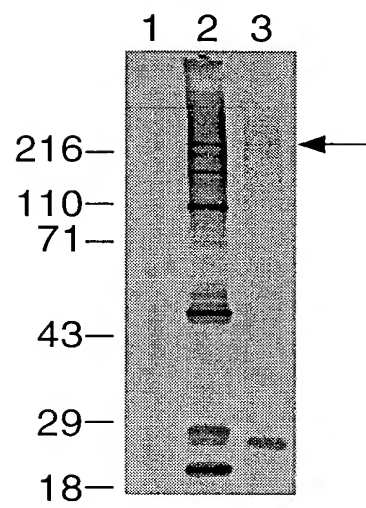


Figure 2

# Polycistronic Constructs

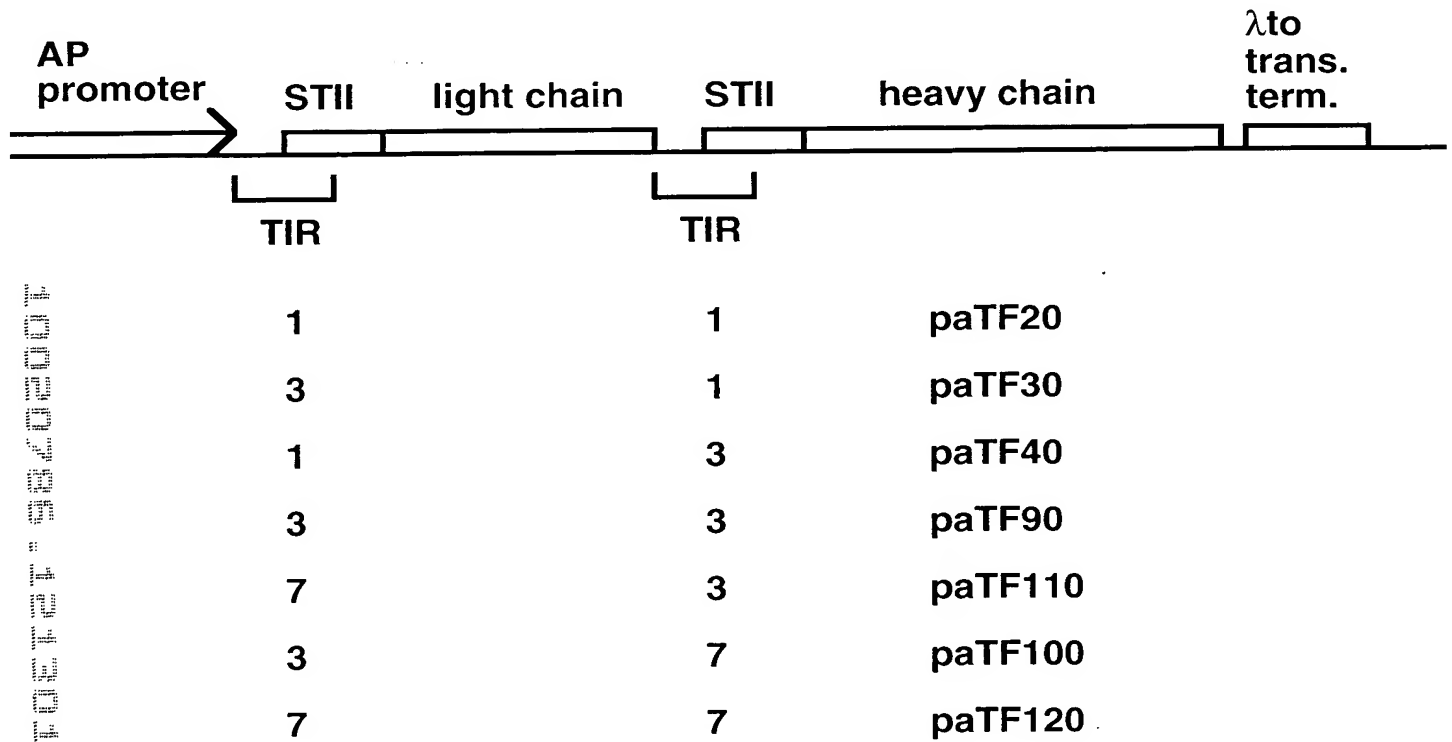


Figure 3.

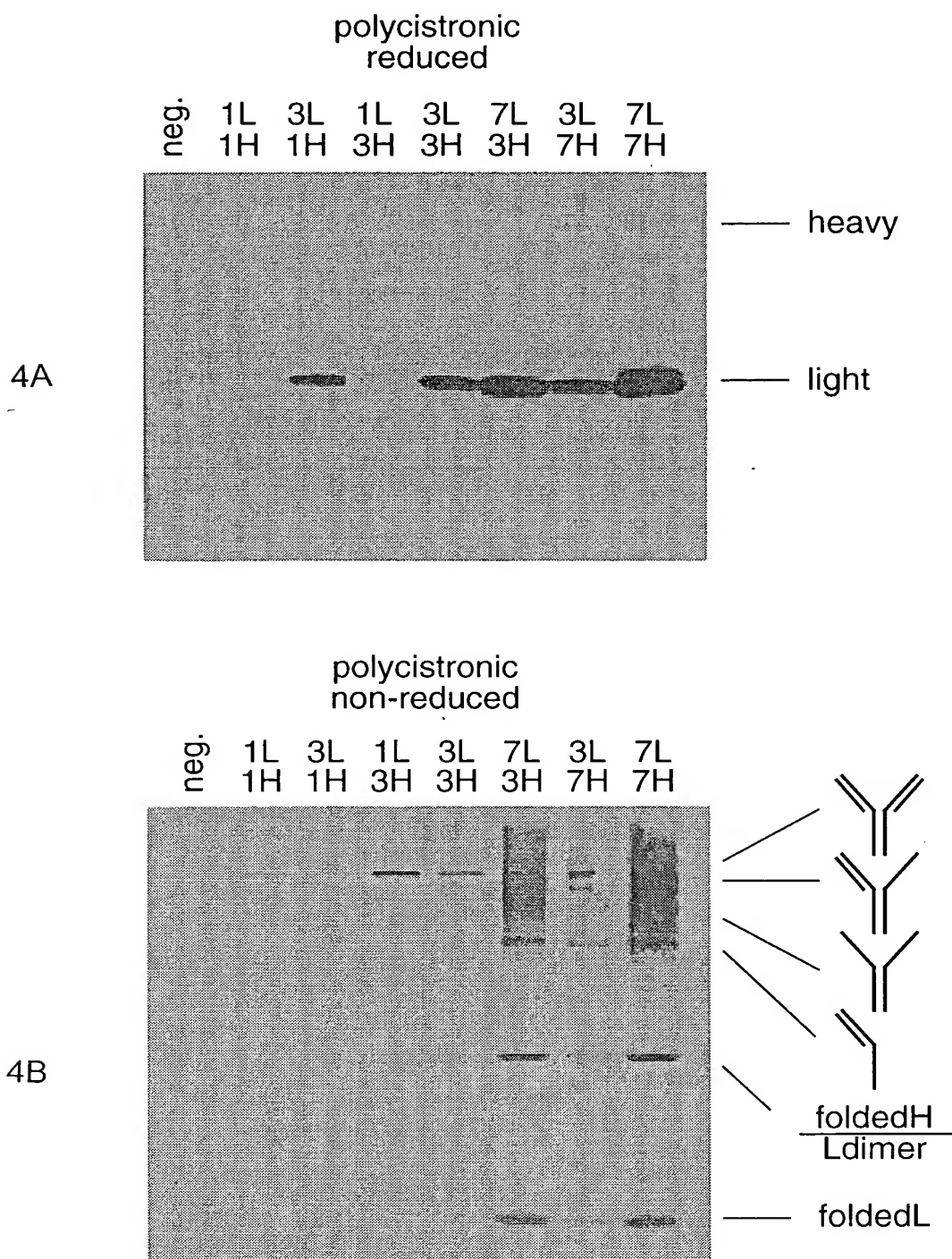
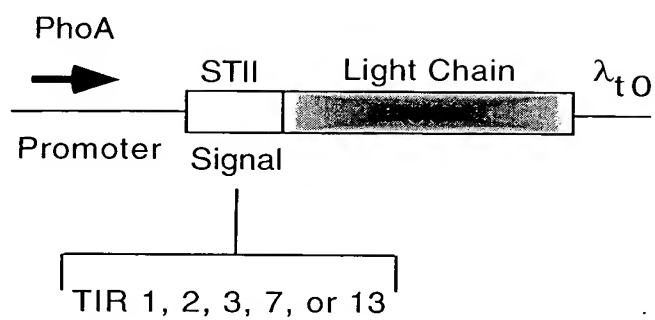


Figure 4

### Light Chain Constructions



### Heavy Chain Constructions

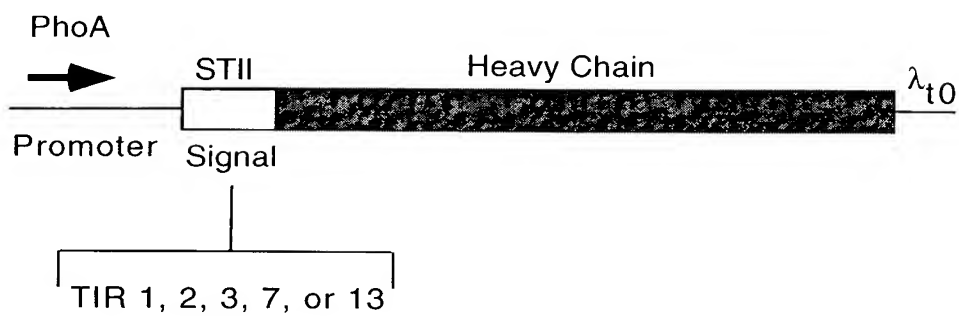


Figure 5

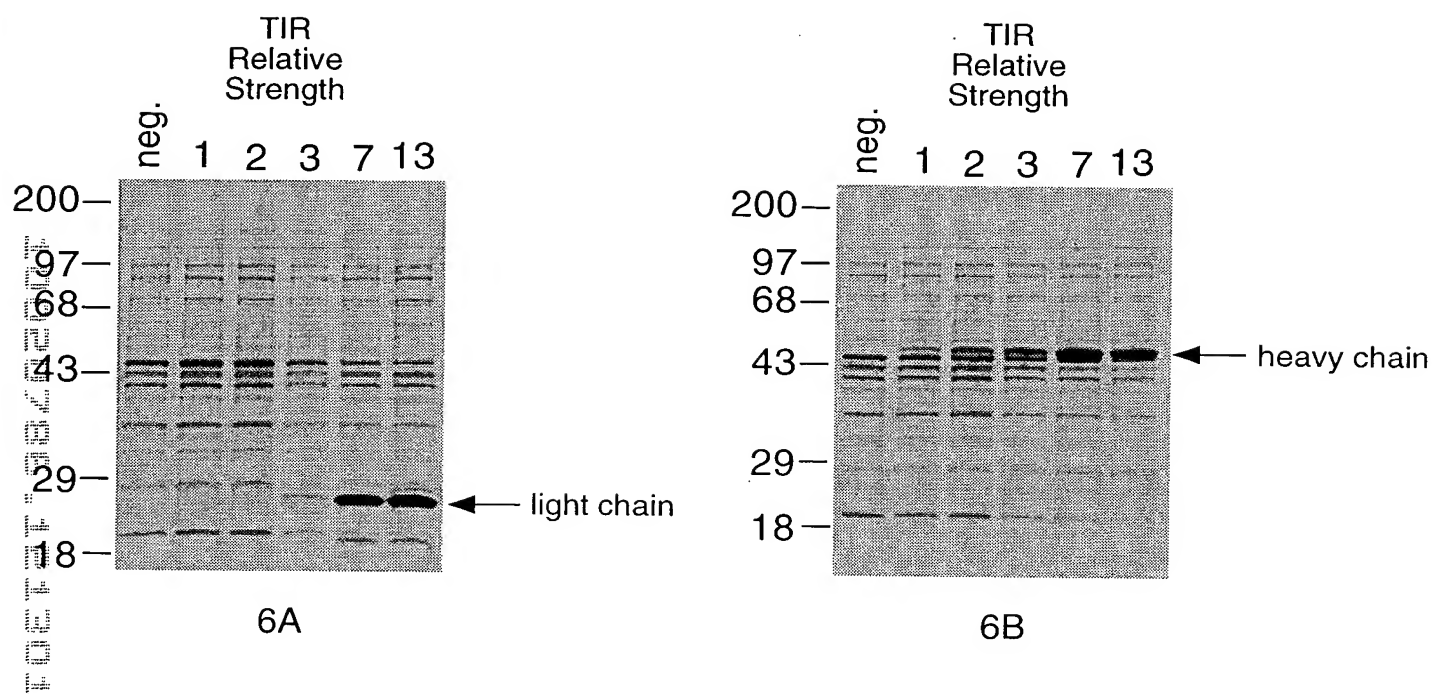


Figure 6

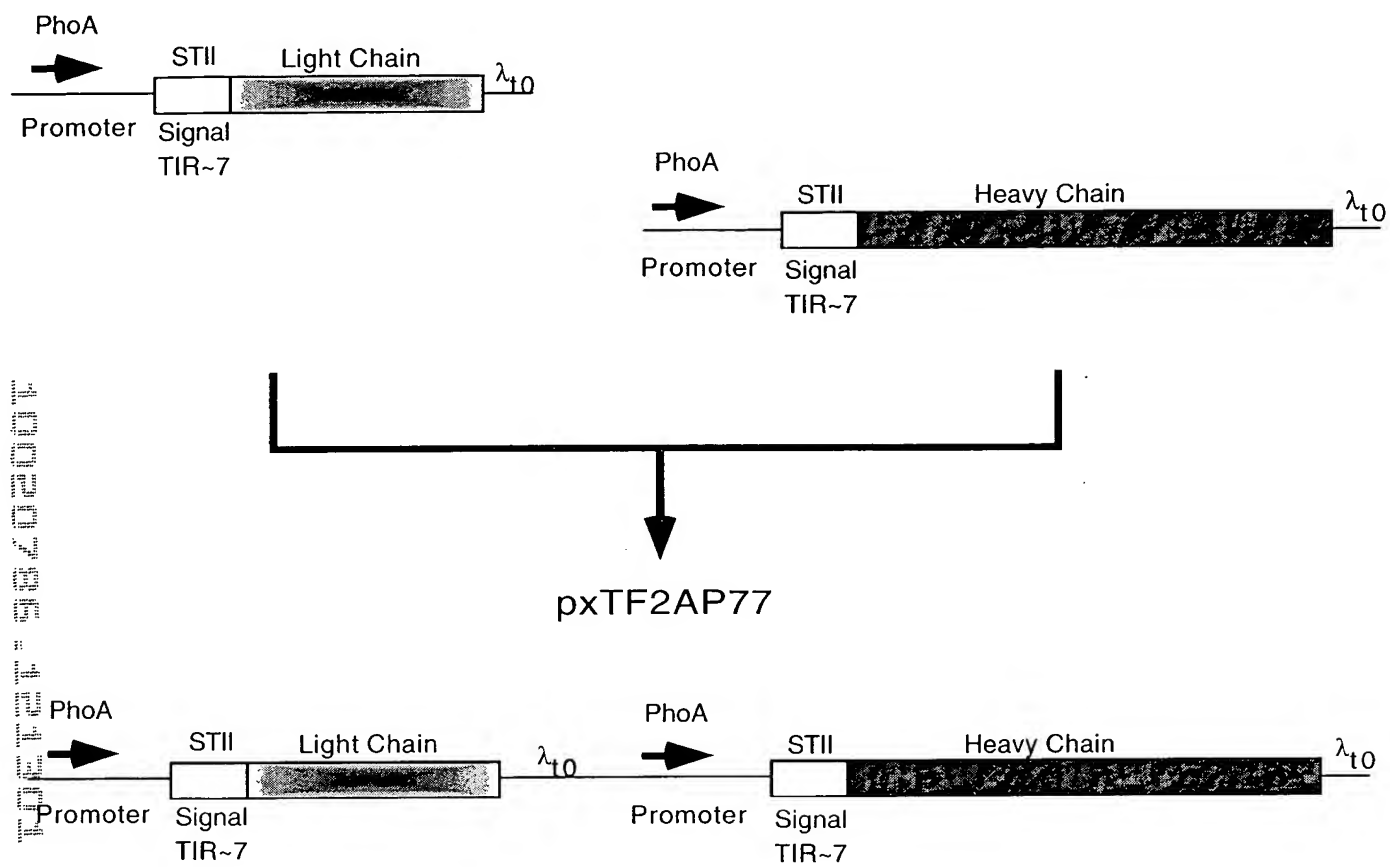


Figure 7

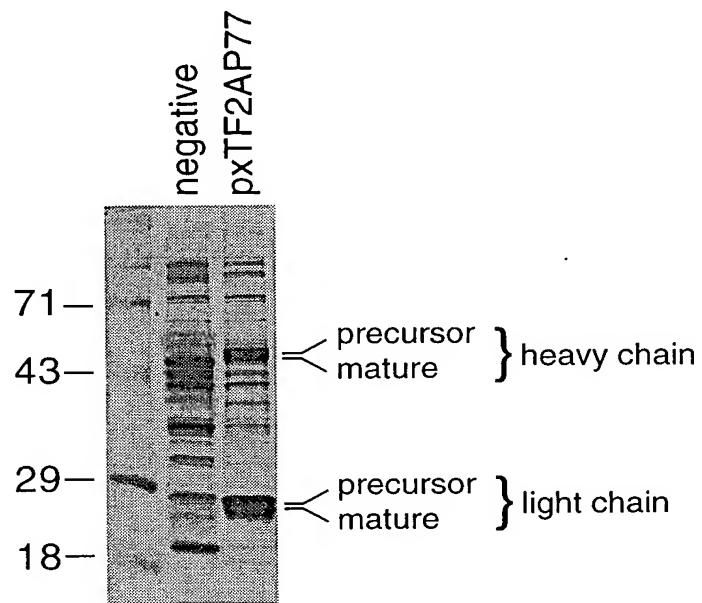


Figure 8



## Separate Cistron Constructs

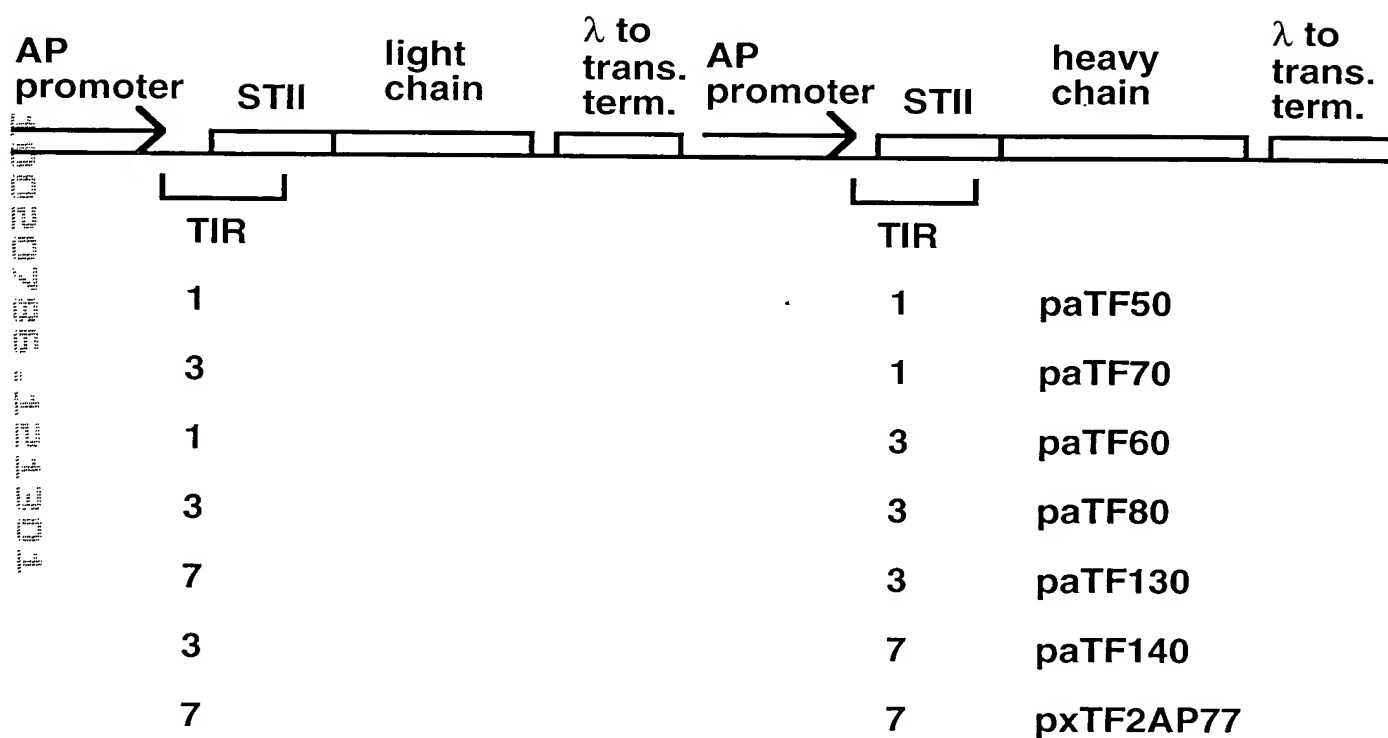


Figure 9

TOPP-926000T

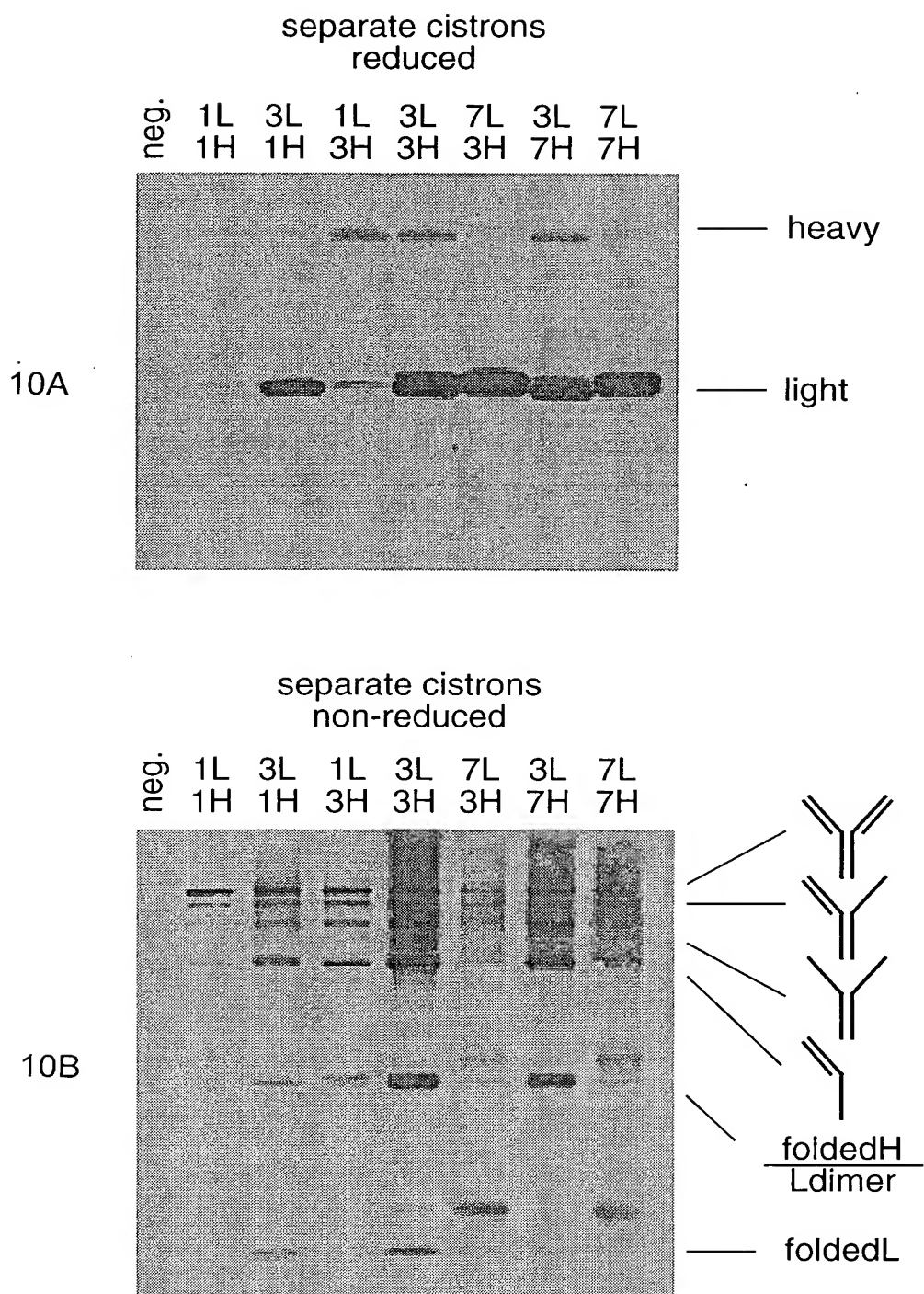
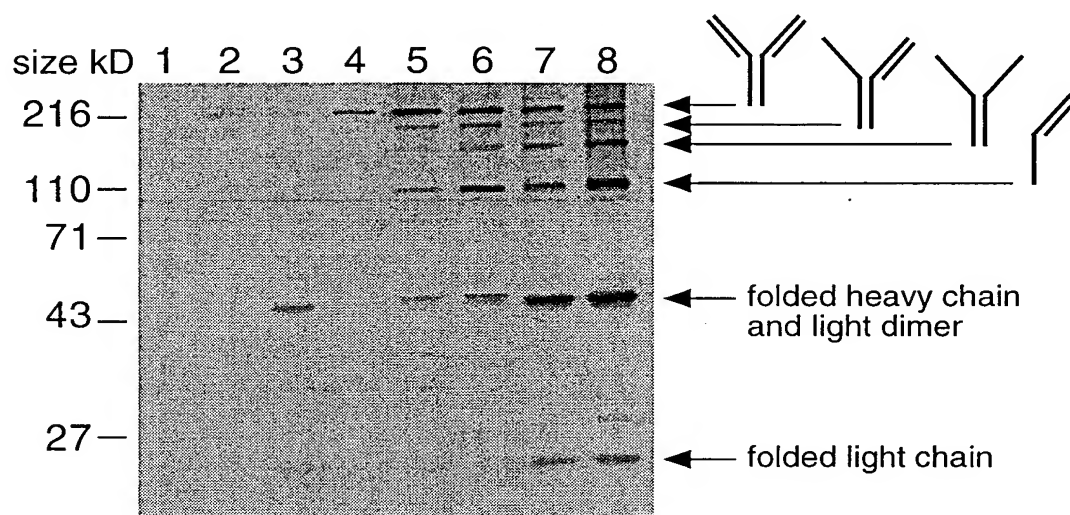


Figure 10



- 1) negative control
- 2) TIR 1-light, TIR 1-heavy, polycistronic
- 3) TIR 3-light, TIR 1-heavy, polycistronic
- 4) TIR 1-light, TIR 3-heavy, polycistronic
- 5) TIR 1-light, TIR 1-heavy, separate cistrons
- 6) TIR 1-light, TIR 3-heavy, separate cistrons
- 7) TIR 3-light, TIR 1-heavy, separate cistrons
- 8) TIR 3-light, TIR 3-heavy, separate cistrons

Figure 11

1000936-1301

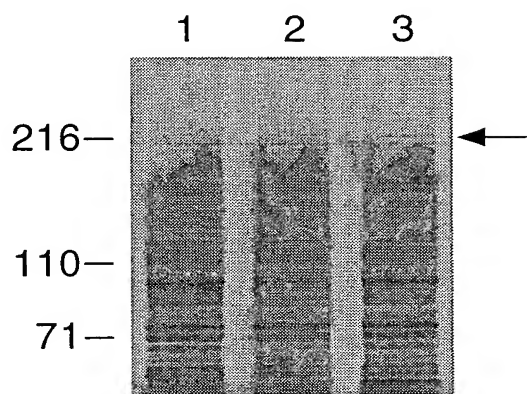


Figure 12

SDS-PAGE gel showing protein profiles. Lane 1: Molecular weight markers (216, 110, 71, 43, 29, 18 kDa). Lane 2: E. coli strain 100. Lane 3: E. coli strain 100 + 100 μg/ml tetracycline. An arrow points to a band at approximately 216 kDa in lane 3.

Figure 13

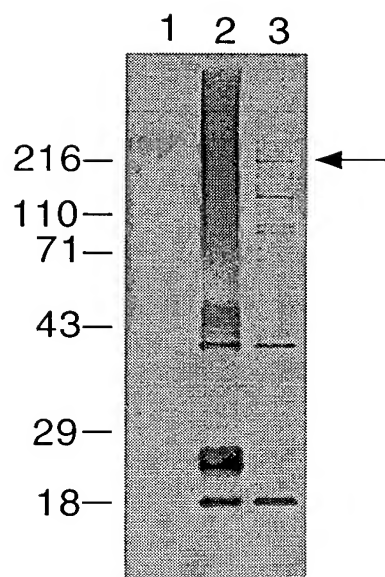
[illegible]

Figure 14



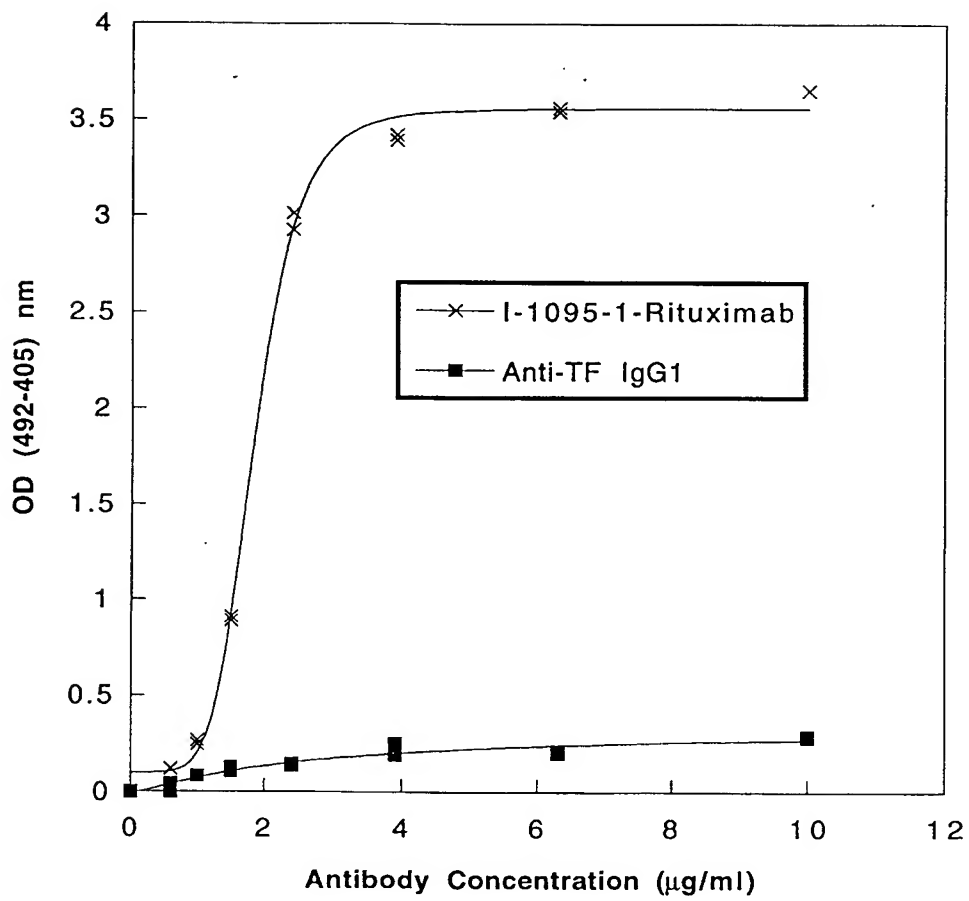


Figure 16



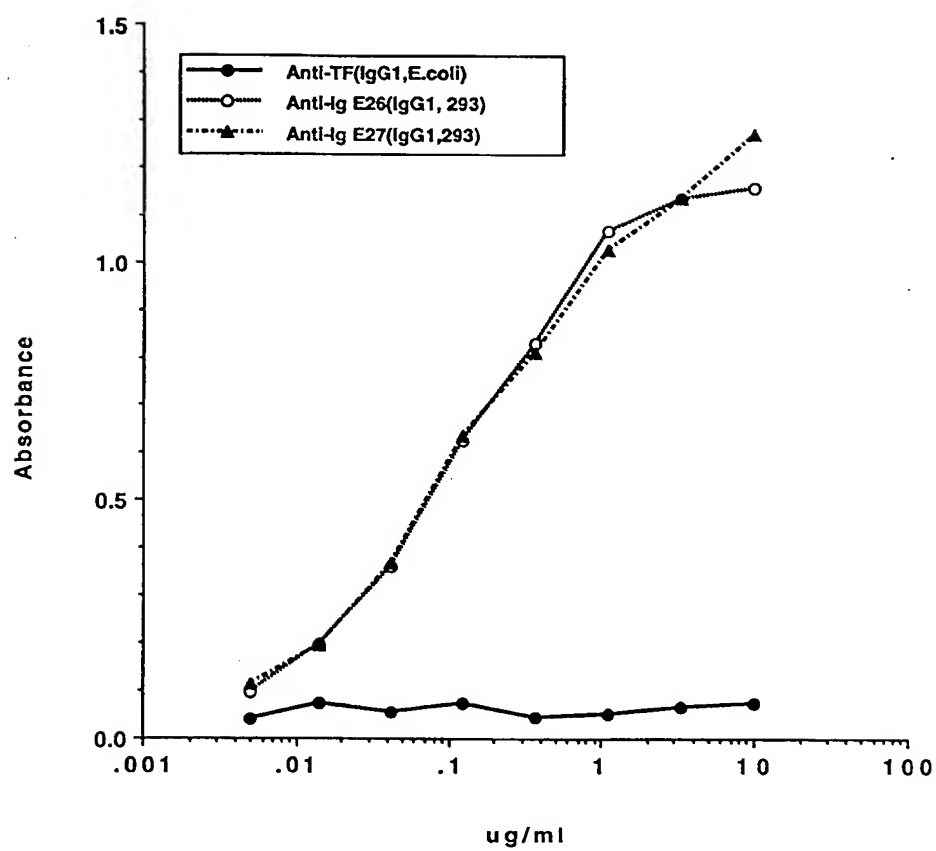


Figure 17

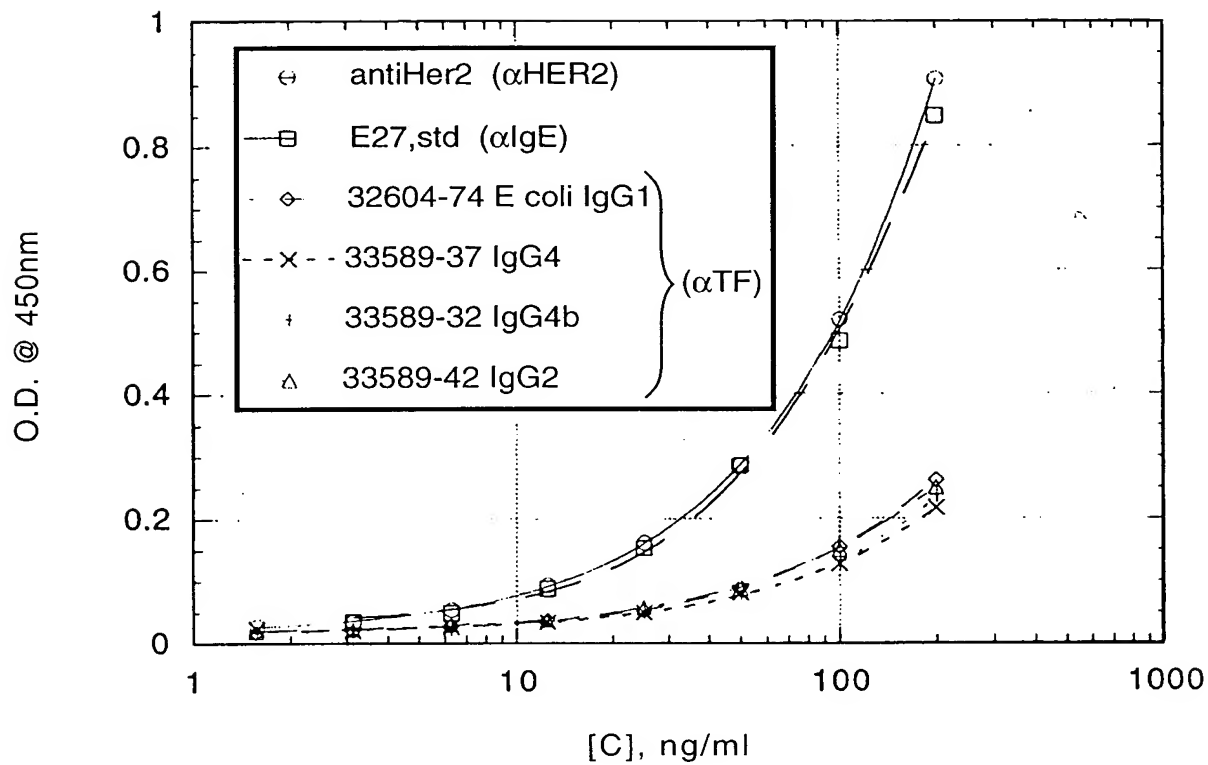


Figure 18

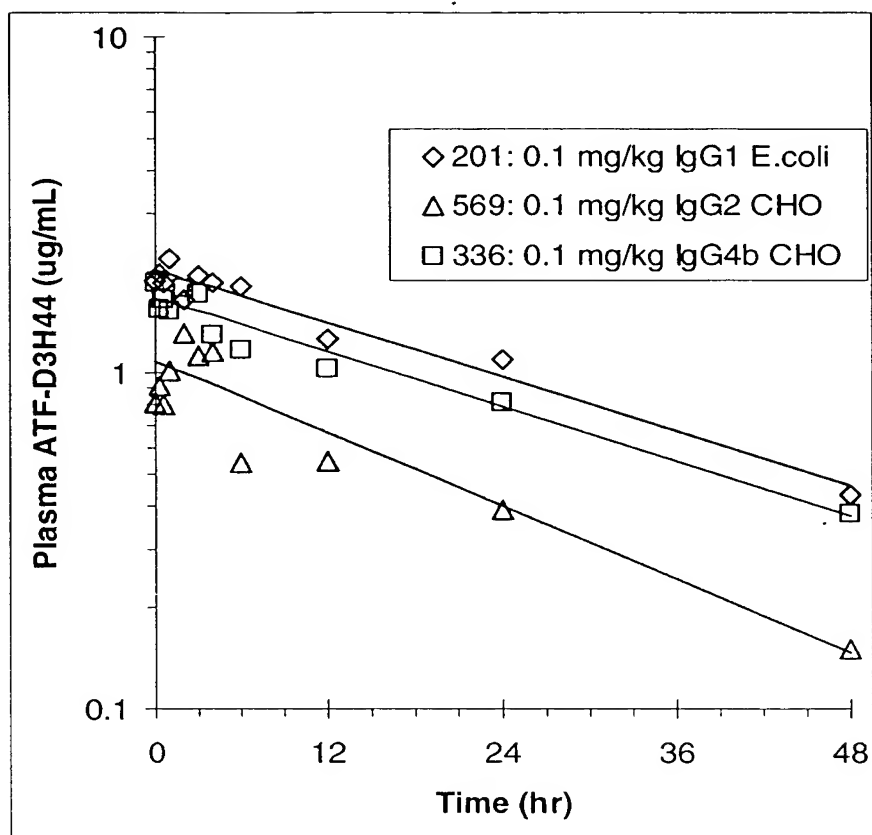


Figure 19

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CTTAAGTTGA AGAGGTATGA AACCTATTCC TTTATGCTG TACTTTTAG AGTAACGACT CAACAATAAA TTGGAACGGG TTTTCTTCT TCTCAGCTTA

101 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GGCAGAAATG ACCAACACGG GTTGATTGAT CAGGTAGAGG  
CTTCACACAC GCGTCCATCT TCGAATCCCT TAATAGCAGT GACGTTACGA AGCGTTATAC CGCGTTTAC TGGTTGTCGC CAACTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCTCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA  
CCCGCGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGACG CGCTAATGCA TTTCTTCAAT AACTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTCAACA GCTGTCAATA AGTTGTACAG GCCGAGACTT ATAGTCGCTT TGTCTTATTT TTTTAACTA TTGTAACTA GTACGCAAGT  
TTTTCRAATTA GAAAGTTGT CGACAGTATT TCAACAGTGC CGGCTCTGAA TATCAGCGAA ACAAATAAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCAGTAAAA AGGTATCTA GAATTATGAA GAAGAATATC GCATTCTTTC TTGCATCTAT GTTCGTTTTI TCTATTGCTA CAAACGCGTA CGCTGATATC  
AGTGCAATTTT TCCCATAGAT CTTAATACTT CTTCTTATAG CGTAAGAAG AACGTAGATA CAAGCAAAA AGATAACGAT GTTTCGCCAT GCGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I  
Anti-Tissue Factor Light Chain\*

^STII Signal Sequence TIR-1

501 CAGATGACCC AGTCCCGAG CTCCTGTGCC GCCTGTGTGG GCGATAGGT CACCATCACC TGCAGAGCCA GTCCGACAT CAAGAGCTAT CTGAACCTGGT  
GTCTACTGGG TCAGGGGCTC GAGGACAGG CGGAGACACC CGCTATCCCA GTGGTAGTG ACCTCTCGGT CAGCGCTGTA GTTCTCGATA GACTTGACCA

26 Q M T Q S P S L S A S V G D R V T I T C R A S R D I K S Y L N W Y

601 ATCAACAGAA ACCAGGAAA GCTCCGAAAG TACTGATTTA CTATGCTACT AGTCTGCTG AAGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGAC  
TAGTGTCTT TGGTCTTTT CGAGCTTTC ATGACTAAT GATACATGA TCAGAGCGAC TTCTCAGG AGAGCGAAG AGACTAGGC CAAGACCTG

60 Q Q K P G K A P K V L I Y A T S L A E G V P S R F S G S G T

701 GAATTACACT CTGACCATCA GCAGTCTGCA GCCAGAGAC TTGCAACTT ATTACTGTCT TCAGCAGCGA GAGTCTCCAT GGACATTGG ACAGGTACC  
CCTAATGTGA GACTGTAGT CGTCAGAGT CGGTCTTCTG AAGCGTTGAA TAATGACAGA AGTCGTGCTCT CTCAGAGTA CCTGTAACC TGTCCTATGG

93 D Y T L T I S S L Q P E D F A T Y Y C L Q H G E S P W T F G Q G T

801 AAGGTGGAGA TCAACGAAAC TGTGGCTGCA CCATCTGTCT TCACTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCTGC  
TTCCACCTCT AGTTTCTTG ACACCGACST GGTAGACAGA AGTAGAAGG CGGTAGACTA CTGCTCAACT TTAGACCTTG ACGAAGACAA CACACGACG

126 K V E I K R T V A A P S V F I F P P S D E Q L K S G T A S V V C L L

901 TGAATAACTT CTATCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT CGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA  
ACTTATTGAA GATAGGTCT CTCCGTTTC ATGTCACCTT CCACCTATTG CGGAGGTTA GCCCATGAG GGTCTCTCA CAGTGTCTCG TCCTGCTGTT

160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K

1001 GGACAGACC TACAGCTCA GCAGCACCT GAGCTGAGC AAAGCAGACT AGGAGAAACA CAAAGTCTAC GCTCGGAAG TCACCCATCA GGGCTGAGC  
CCTGCTGG AGTGTGAGT GTGCTGGGA CTGCGACTCG TTTCTGCTGA TGTCTTGT GTTTCAGAT CGGAGCTTC AGTGGTAGT CCGGACTCG

193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S

1101 TCGCCCTCA CAAAGAGCTT CAACAGGGGA GAGTGTAAAT TAAATCTCT AGCCGAGG CATCTGGG AGCTCGGTAC CCGGGATCT AGGCTTAACG  
AGCGGAGT GTTCTCGAA GTGTCCCTCT CTCACATTA ATTTAGAGA TCGGCTGTC GTAGCACCG TCGAGCCATG GGGCCCTAGA TCGGATTGC

226 S P V T K S F N R G E C O

Figure 20a

1201 CTCGGTTGCC GCGGGCGTT TTTTATTGT GCGAGCGC ATCTGAATG AACTGTGTGC GCAGTAGAA GCTTTGGAGA TTATCGTAC TGCAATGCTT  
GAGCAAGG CGGCCGCA AATTAACAA CCGCTGCGG TAGAGCTTAC TTGACACAG CGTCCATCTT CGAAACCTCT AATAGCAGTG ACGTTAGAA

1301 CGCAATATGG CGCAAAATGA CCAACAGCGG TTGATTGATC AGTAGAGGG GCGGTGTATC GAGTAAAGC CCGATGCCAG CATTCGTAC GAGCATACGG  
GCGTTATACC GCGTTTACT GGTGTGCGC AACTAACTAG TCATCTCCC CCGGACATG CTCATTTCC GGTACGGTC GTAAGGACTG CTGCTATGCC

1401 AGCTGCTGCG CGATTACGTA AAGAAGTTAT TGAAGCATCC TGTTCAGTAA AAGTTAATC TTTTCAACAG CTGTCAATAA GTTGTACCG CCGAGACTTA  
TCGAGGAGCG GCTAATGCAT TTCTTCAATA ACTTGTAGG AGCAGTCAT TTTCATTTAG AAAATTGTC GACAGTATTT CAACAGTCCC GGCTCTGAAT

1501 TAGTGGCTTT GTTTTATTT TTTAATGTAT TTGTAACATG TAGGCAAGTT CAGTAAATAA GGGTAATCTAG AATTATGAAG AAGAATATCG CATTTCTTCT  
ATCAGCGAAA CAAAATAAAA AAATTACATA AACATTGATC ATCGGTTCAA GTGCATTTT CCATAGATC TTAATACTTC TTCTATAGC GTAAAGAAGA  
M K K N I A F L L  
\*STII Signal Sequence TIR-1

1601 TGCAATCTATG TTGTTTCTTT CTATTGCTAC AAACGGGTAC GCTGAGTTTC AGCTGTGTGA GTCTGGCGGT GGCCTGTGTC AGCCAGGGG CTCACTCCGT  
ACGTAGATAC AAGCAAAAA GATAACGATG TTTGGCATG CGACTCCAG TCGACCACCT CAGACCGCCA CCGGACCAG TCGTCCCCC GAGTGGGCA  
10 A S M F V F S I A T N A Y A E V Q L V E S G G L V Q P G S L R  
\*Anti-Tissue Factor Heavy Chain

1701 TTGTCTGTG CAGTTCTCG CTTCAATATT AAGAGTACT ACATGACTG GTCGCTCAG GCCCGGGA AGGGCTTGA ATGGTTTGA TTGATTGATC  
AACAGGACAC GTCAAGACC GAAGTTATAA TTCTCATGA TGTAGTGCAC CCAGCGATC CCGGGCCCAT TCCCGACCT TACCAACCT AACTAACATG  
43 L S C A A S G F N I K E Y Y M H W V R Q A P G K G L E W V G L I D P

1801 CAGAGCAAGG CAACAGATC TATGACCGA AGTTCCAGGA CCGTGCCACT ATAAGCGCTG ACAATTCOA AACACAGCA TACCTGCAGA TGAACAGCCT  
GTCTCGTTCC GTTGCTAG ATACTGGCT TCAAGTCTT GGACGGTGA TATTGCGAC TGTAAAGTT TTTGTGTGT ATGACGCTCT ACTTGTGGA  
77 E Q G N T I Y D P K F Q D R A T I S A D N S K N T A Y L Q M N S L

1901 GCGTGCTGAG GACACTGCG TCTATTATG TGTTCGAGAC ACGGCGCTT ACTTCGACTA CTGGGTGCA GGAACCTGG TCACGCTCT CTGGGCTCC  
CGCAGACTC CTGTGACGCG AGATAAATAC ACGAGTCTG TGCCGCGGAA TGAAGTGTAT GACCCGATT CCTTGGGACC AGTGGCAGAG GAGCCGGAGG  
110 R A E D T A V Y Y C A R D T A A Y F D Y W G Q G T L V T V S S A S

2001 ACCAAGGGCC CATCGTCTT CCCCCTGGCA CCTCTCTCA AGAGCACCTC TGGGGGACA GCGGCCCTGG GCTGCTGTG CAAGGACTAC TTCCCGGAAC  
TGGTTCCCG GTAGCCAGAA GGGGACCGT GGGAGGAGT TCTGTGAG ACCCCCGTGT CCGCGGACC CGACGACCA GTTCTGTATG AAGGGCTTG  
143 T K G P S V F P L A P S S K S T S G G T A A L G C L V K D Y F P E P

2101 CGGTGACGT GTGTGGAAC TCAGCGGCC TGACCAAGCG CGTGCACAC TTCCGGGTG TCCTACAGTC CTCAGGACTC TACTCCCTCA GCAGCGTGGT  
GCCACTGCC CAGCACCTTG AGTCGCGG ACTGTGCGC GCAGGTGTG AAGGCCGAC AGATGTGAG GAGTCTGAG GAGTCTGAG Y S L S S V V  
177 V T V S W N S G A L T S G V H T F P A V L Q S S G L Y S L S S V V

2201 GACTGTGCC TCTAGAGCT TGGGACCCA GACCTACATC TGCAAGTGA ATCAAGCC CAGCAACACC AAGGTGGACA AGAAAGTTGA GCCAAATCT  
CTGACACGG AGATCGTCA ACCGTGGGT CTGGATCTAG ACGTTGCACT TAGTGTTCGG GTCGTTGTTG TTCCACCTGT TCITTTCACT CGGTTTGA  
210 T V P S S S L G T Q T Y I C N V N H K P S N T K V D K K V E P K S

2301 TGTGACAAA CTCACATG CCCACGTC CCAGCACTG AACTCTGG GGGACCGTCA GTCTTCTCT TCCCCCAAA ACCCAAGAC ACCCTCATGA  
ACACTGTTT GAGTGTGTAC GGTGGCAG GTCTGTGAC TTGAGACCC CCCTGGCAGT CAGAAGAGA AGGGGGTTT TGGGTTCCTG TGGGAGTACT  
243 C D K T H T C P P C P A P E L L G G P S V F L F P P K P K D T L M I

2401 TCTCCCGGAC CCTGAGGTC ACATGCGTGG TGTGAGCT GAGCACGAA GACCTGAG TCAAGTTCAA CTGGTACGT GACGCGTGG AGGTGCATAA  
AGAGGCGCTG GGGACTCCAG TGTAGCACC ACCACTGCA CTCGTTGCTT CTGGGACTCC AGTTCAAGTT GACCATGAC CTGCGGACC TCCACGTATT  
277 S R T P E V T C V V V D V S H E D P E V K F N W Y V D G V E V H N

Figure 20b

2501 TGCCNAGACA AAGCCGCGGG AGGAGCAGTA CAACAGCAGG TAGCGTGTGG TCAGGTCCTT CACCGTCCTG CACGAGGACT GGCTGAATGG CAAGGAGTAC  
ACGGTTCTGT TTGCGCGCC TCCTCGTCAT GTTGTCTGTC ATGGCACACC AGTCGACAGA GTGGCAGGAC GTGGTCCTGA CCGACTTACC GTTCCTCATG  
310 A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W L N G K E Y  
2601 AAGTGCAAGG TCTCCNACAA AGCCTCCCA GCCCCATCG AGAAACACAT CTCANAGCC AAAGGCGAGC CCGGAGAACC ACAGGTGTAC ACCCTGCCCC  
TTACGTTCC AGAGGTTGT TCGGAGGGT CGGGGGTAGC TCTTTTGTA GAGTTTCGG TTTCCTCTCG GGGCTCTTGG TGTCACATG TGGGACGGGG  
343 K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q V Y T L P P  
2701 CATCCCGGA AGAGATGACC AAGAACAGG TCAGCTGAC CTGCTGTGTC AAGGCTTCT ATCCAGCGA CATCCCGTG GAGTGGGAGA GCATGGGCA  
GTAGGGCCCT TCTCTACTGG TTCTGTGTC AGTCGACTG GACGACACAG TTTCGGAAGA TAGGTCGCT GTAGCGGCAC CTCACCTCT CGTTACCCGT  
377 S R E E M T K N Q V S L T C L V K G F Y P S D I A V E W E S N G Q  
2801 GCCGGAGAAC AACTACAAGA CCAGCCCTCC CGTGCTGGAC TCGGACGGCT CTTCTTCTCT CTACAGCAG CTACCGGTGG ACAGAGCAG GTGGCAGCAG  
CGGCTCTTGT TTGATGTTCT GGTGCGAGG GCACGACCTG AGGCTGCCGA GGAAGAAGGA GATGTCTTTC GAGTGGCACC TGTTCTCTGTC CACCGTCGTC  
410 P E N N Y K T T P P V L D S D G S F F L Y S K L T V D K S R W Q Q  
2901 GGGACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC ACAACCACTA CACGAGAG AGCCTCTCCC TGCTCTCGGG TAAATAAGCA TGGGACGGCC  
CCCTTGACA AGAGTACGAG GCACTACGTA CTCGAGACG TGTGTGTGAT GTGGTCTTC TCGGAGAGGG ACAGAGGCC ATTTATTCTG ACCTGCCGG  
443 G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K O  
3001 CTAGAGTCCC TAACGTCGG TTGCGCGCGG GCGTTTTTTA TTGTTAACTC ATGTTTGACA GCTTATCATC GATAAGCTTT AATGCGGTAG TTTATCACAG  
GATCTCAGG ATTGCGAGC AACGGCGGCC CGCAAAAAAT AACAATTGAG TACAACCTGT CGAATAGTAG CTAATTCGAAA TTACGCCATC AATAGTGTG  
3101 TTAATTGCT AACGCAGTCA GGCACCGTGT ATGAATCTA ACAATCGCT CATGTCATC CTCGACCGG TCACCTTGA TCCTGTAGGC ATAGGCTTGG  
AATTTAACA TTGCGTCAGT CCGTGGCACA TACTTTAGAT TGTTAGCGA GTAGCAGTAG GAGCGGTGG AGTGGGACCT ACGACATCCG TATCCGAACC  
~Start Tet Resistance Coding Sequence  
3201 TTATGCGGT ACTGCCGGG CTCTTGCGG ATATCGTCA TTCCGACAGC ATGCCAGTC ACTATGCGT GCTGTAGCG CTATATCGT TGATGCAATT  
AATACGGCCA TGACGCGCGG GAGAACGCC TATAGCAGT AAGGCTGTG TAGCGGTGAG CGACCATCG GATATACGCA ACTACGTTAA

3301

Figure 20c

# Figure 21a

1 GAATTCAACT TCTCCACT TTGGATAAGG AAATACAGAC ATGAAAAATC TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT  
CTTAAGTTGA AGAGGTATGA AACCTATTCC TTATATGCTG TACTTTTATG AGTAAGGACT CAACAATAAA TTGCAACGGG TTTTCTTCTT TCTCAGCTTA

101 GAACCTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT TCGCAATATG GCGCAAAATG ACOACACAGG GTTGATTGAT CAGGTAGAGG  
CTTGACACAC GCGTCCATCT TCGAAACCTC TAATAGCAGT GACGTTACGA AGCGTTATAC CCGCTTTTAC TGGTTCTGCG CAACTAACTA GTCCATCTCC

201 GGGCGCTGTA CGAGGTAAG CCCGATGCCA GCAITTCCTGA CGACGATACG GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCACTA  
CCCCGGACAT GCTCCATTTC GGGCTACGGT CGTAAGGACT GCTGCTATGC CTCGACGAGC CGTAATGCA TTTCTTCAAT AACCTTCGTAG GAGCAGTCAT

301 AAAAGTTAAT CTTTTCNACA GCTGTCAATAA AGTTGTACAG GCGAGACTT ATAGTCGCTT TGTTTTATTT TTTTAAATGA TTGTAACTA GTACGCAAGT  
TTTTCAATTA GAAAAGTTGT CGACAGTATT TCAACAGTGC CGCTCTGAA TATCAGCGAA ACAAAATAA AAAATTACAT AAACATTGAT CATGCGTTCA

401 TCACGTAAAA AGGTATCTTA GAATTATGAA GAAGATATC GCATTTCTTC TTGCATCTAT GTTCGTTTTT TCTATTGCTA CAAACGCGTA CGCTGATATC  
AGTGCATTTT TCCCATAGAT CTTAATACTT CTTCTTATAG CGTAAGAAG AACGTAGATA CAACCAAAAA AGATAACGAT GTTTGCGAT GCGACTATAG

1 M K K N I A F L L A S M F V F S I A T N A Y A D I  
^STII Signal TIR -1 Anti-VESF Light chain^

501 CAGTTGACCC AGTCCCGGAG CTCCTCTGCC GCCTCTGTGG GCGATAGGGT CACCATCACC TGCAGCGCAA GTACAGATAT TAGCAACTAT TTAACCTGGT  
GTCAACTGGG TCAGGGGCTC GAGGACACAG CGCTATCCCA GTGGTAGTGG ACGTCGCGTT CAGTCCCTATA ATCGTTGATA AATTGACCA

26 Q L T Q S P S S L S A S V G D R V T I T C S A S Q D I S N Y L N W Y

601 ATCAACAGAA ACCAGGAAGA GCTCCGAAG TACTGATTTA CTTCACTCC TCTCTCCACT CTGGAGTCCC TTCTGCTTC TCTGATCCG GTTCTGGGAC  
TAGTTGTCTT TGGTCTCTTT CGAGGCTTTC ATGACTAAAT GAAGTGGAGG AGAGAGGTGA GACCTCAGG AGAGCGAAG AGACCTAGGC CAAGACCTG

60 Q Q K P G K A P K V L I Y F T S S L H S G V P S R F S G S G S G T

701 GGATTTCACT CTGACCATCA CGAGTCTGCA GCGAGAAGAC TTGCGCAACT ATTACTGTCA ACAGTATAGC ACCGTGCCGT GGAGGTTTGG ACAGGATACC  
CCTAAAGTGA GACTGTAGT GGTACAGAGT CGGTCTTCTG AAGCGTTGAA TAATGACAGT TGTCATATCG TGGCAGCGCA CCGCAAAACC TGTCCTCATGG

93 D F T L T I S S L Q P E D F A T Y Y C Q Q Y S T V P W T F G Q G T

801 AAGGTGAGA TCAACGAACT TGTGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCTGTC  
TTCCACCTCT AGTTTGTCTG ACACCGAGCT GGTAGACAGA AGTAGAAGG CGGTAGACTA CTGCTCAACT TTAGACCTTG ACAGAGACAA CACACGAGC

126 K V E I K R T V A A P S V F I F P S D E Q L K S G T A S V V C L L

901 TGAATACTT CTATCCCA GAGGCCAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT CCGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA  
ACTTATTGAA GATAGGTTCT CTCCGGTTTC ATGTCACCTT CCACCTATTG CCGGAGGTGA GCCCATTTAG GGTCTCTCA CAGTGTCTCG TCCTGTCTGTT

160 N N F Y P R E A K V Q W K V D N A L Q S G N S Q E S V T E Q D S K

1001 GGACAGCACC TACAGCCTCA CGAGCACCTT GACGCTGAGC AAAGCAGACT ACAGAAACA CAAAGTCTAC GCGTGGAG TCACCCATCA GGGCTGAGC  
CCTGTCTGG ATGTGCGAGT CGTGTGGGA CTGCGACTCG TTTCTGCTGA TGCTTTTGT GTTTCAGATG CCGAGCTTC AGTGGGTAGT CCGGACTCG

193 D S T Y S L S S T L T L S K A D Y E K H K V Y A C E V T H Q G L S

1101 TCGCCCGTCA CAAAGAGCTT CAACAGGGA GAGTGTAAAT TAAATCTCTT ACGCGGAGC CATCTGTGGG AGCTCGGTAC CCGGGGATCT AGGCTTAAGC  
AGCGGGCAGT GTTCTCGAA GTTGTCCCT CTCAATTA ATTAGAGA TCGCGCTGTC GTAGCACCGC TCGAGCCATG GGGCCCTAGA TCCGATTGC

226 S P V T K S F N R G E C O

Figure 21a

1201 CTCGGTGGCC GCGGGCGTT TTTTATTGT GCCGACGGC ATCTCGAATG AACTGTGTGC GCAGTAGAA GCTTTGGAGA TTATGTCAC TGCAATGCTT  
GAGCCACGG CGGCCCGCAA AAAATAACAA CCGCTGGCG TAGAGTTAC TTGACACAG CGTCCATCTT CGAAACCTCT AATAGCAGTG ACGTTACGAA

1301 CGCATATGG CGCAAAATGA COACACGGG TTGATTGATC AGTAGAGGG GCGCTGTAC GAGTAAAGC CCGATGCCAG CATTCCTGAC GACGATACGG  
GCGTTATACC GCGTTTACT GGTGTGCGC AACTAAGTAG TCCATCTCCC CCGGACATG CTCCATTTTC GGTACGGTC GTAAGGACTG CTGCTATGCC

1401 AGCTGCTGCG CGATTAGCTA AAGAAGTTAT TGAAGCATCC TCGTCAGTAA AAGTTAATC TTTTCAACAG CTGTCAATAA GTTGTACGG CGGAGACTTA  
TCGAGGAGCG GCTAATGCAT TTCITCAATA ACTTCGTAGG AGCAGTCAIT TTTCATTAG AAAAGTTGTC GACAGTATTT CAACAGTGCC GGTCTCTCAAT

1501 TAGTCGGCTTT GTTTTATTAT TTTAATGTAT TTGTAAGTAG TAGCAAGTT CAGCTAAATA GGTATCTAG AATTATGAG AAGAATATCG CATTTCTTCT  
ATCAGCGAAA CAAAATATAA AAATTACATA AACATTGATC ATGCGTTCAA GTGCATTTT CCATAGATC TTAATACTTC TTCTTATAGC GTAAAGAAGA  
M K K N I A F L L  
\*STII Signal TIR-1

1601 TGCATCTATG TTCGTTTTTT CTATTGCTAC AAACGCGTAC GCTGAGGTTG AGTGTGTGA GTCTGGCGGT GGCCTGGTGC AGCCAGGGGG CTCACCTCGT  
ACGTAGATAC AAGCAAAAAA GATAACGATG TTTGCGCATG CGACTCCAAG TCGACCACT CAGACCGCCA CCGGACCAAG TCGGTCCCC GAGCTGAGGA  
10 A S M F V F S I A T N A Y A E V Q L V E S G G L V Q P G S L R  
\*Anti-VEGF Heavy Chain

1701 TTGTCCTGTG CAGCTTCTGG CTAGCACTTC AGCACTACG GTATGAATCG GTTCGGTAC GCGCCGGTA AGGGCTTGA ATGGTITGA TGGATTAAAC  
AACAGGACAC GTCGAAGACC GATGCTGAAG TGGCTGATGC CATCTTGAC CCAGCAGTC CCGGGGCCAT TCCCGACCT TACCCAACCT ACCTAATTGT  
43 L S C A A S G Y D F T H Y G M N W V R Q A P G K G L E W V G W I N T

1801 CCTATACCGG TGAACCGACC TATGCTGCGG ATTTCAAAG TCGTTTCACT TTTTCTTTAG ACACCTCCA AAGCACAGA TACCTGCAGA TGAACAGCCT  
GGATATGCC ACTTGCTGG ATAGACGCC TAAAGTTGC AGCAAGTGA AAAAGAAATC TGTGGAGTT TCTGTGTCGT ATGACGCTCT ACTTGTGCGA  
77 Y T G E P T Y A A D F K R R F T F S L D T S K S T A Y L Q M N S L

1901 GCGGCTGTAG GACATGCGG TCTATTACTG TGCAAAAGTAC CCGTACTATT AGGCACAGG CCACTGTTAT TTGACGCTCT GGGTCAAG AACCTTGGTC  
CGGCGACTC CTGTGACGGC AGATAATGAC ACGTTTCAATG GGCATGATGA TGCGTGTCTG GGTGACCATTA AAGTGCAGA CCCAGTTCC TTGGGACCAAG  
110 R A E D T A V Y Y C A K Y P Y Y Y G T S H W Y F D V W G Q G T L V

2001 ACCGTCTCCT CGGCTCTCAC CAAGGGCCCA TCGTCTTCC CCGTGGCAC CCGTCTCAAG AGCACCTCTG GGGGCACAGC GGCCTTGGGC TGCCTGGTCA  
TGGCAGAGGA GCGGAGGTG GTTCCCGGT AGCCAGAAG GGGACGCTG GAGGAGTTT TCGTGTGAGC CCGGTGTG CCGGACCCG ACGGACCACT  
143 T V S S A S T K G P S V F P L A P S S K S T S G G T A A L G C L V K

2101 AGGACTACTT CCGCAACCG GTGACGGTGT CGTGGAATC AGGCGCCCTG ACCAGCGGG TGCAACCTT CCGGCTGTCT CTACAGTCTT CAGGACTCTA  
TCTGTATGA GGGCTTGGC CACTGCCACA GCACCTTGA TCGCGGGAC TGGTGGCGG CAGTGTGGA AGTGTGGA GGGCGACAG GATGTGAGA GTCTGTGAT  
177 D Y F P E P V T V S W N S G A L T S G V H T F P A V L Q S S G L Y

2201 CTCCTCAGC AGCTGTGTA CTGTGCCCTC TAGCAGCTTG GGCACCCAGA CCTACATCTG CAACGTGAAT CACAAGCCCA GCAACACCAA GGTGGACCAAG  
GAGGAGTGC TCGCACCACT GACACGGAG ATCGTCGAAC CCGTGGGTCT GGATGTAGC GTTGTACTTA GTTGTGGT CCGTGTGGT CCACCTGTTC  
210 S L S S V V T V P S S S L G T Q T Y I C N V N H K P S N T K V D K

2301 AAAGTTGAGC CCAATCTTG TGCAAAACT CACATATGCC CACGCTGCC AGCACTGAA CTCCTGGGG GACGCTCAGT CTTCCTCTTC CCCCCAAAAC  
TTTCAACTCG GGTITAGAAC ACTGTTTGA GTGTGTACCG GTGGACCGG TCGTGGACTT GAGGACCCCG CTGGCAGTCA GAAGGAGAAG GGGGGTTTTG  
243 K V E P K S C D K T H T C P P C P A P E L L G G P S V F L F P P K P

2401 CCAAGGACAC CCTCATGATC TCCCGGACC CTGAGTCTAC ATGCTGTG GTGACGTGA GCCAGAAGA CCTGAGGTC AAGTTCAACT GGTACGTGGA  
GGTCTCTGTG GGAGTACTAG AGGCTTGG GACTCCAGTG TACGACCCAC CACTGTCACT CCGTCTCTT GGGACTCCAG TTCAAGTTGA CCATGCACCT  
277 K D T L M I S R T P E V T C V V V D V S H E D P E V K F N W Y V D

Figure 21b



2501 CGCGTGGAG GTGCATAATG CCAAGACAAA GCCGCGGGAG GAGCAGTACA ACAGCACGTA CCGTGTGGTC AGGTCTCTCA CCGTCTCTCA CCAGGACTGG  
GCCGACCTC CACGTATTAC GGTTCGTGTT CGGCGCCCTC CTCGTGATGT TGTCTGTCAT GGCACACAG TCGCAGGAGT GGCAGGAGT GGTCTCTGACC  
310 G V E V H N A K T K P R E E Q Y N S T Y R V V S V L T V L H Q D W

2601 CTGAATGGCA AGGAGTACAA GTGCAAGGTC TCCAACAAG CCTCTCCAGC CCCCATCGAG AAAACCATCT CCAAGGCCAA AGGCAGGCC CGAGAACAC  
GACTTACCGT TCCTCATGTT CACGTTCAG AGTTGTGTT GGGAGGTGCG GGGGTAGCTC TTITGGTAGA GGTTCGGTT TCCCGTCGG GCTCTTGGTG  
343 L N G K E Y K C K V S N K A L P A P I E K T I S K A K G Q P R E P Q

2701 AGTGTACAC CCTGCCCCCA TCCCGGGAAG AGATGACAA GAACAGGTC AGCTGACTC GCTGTGCTAA AGCTTCTAT CCCAGCGACA TCGCGGTGGA  
TCCACATGTG GGAGGGGGT AGGCGCCCTC TCTACTGTT CTGTGTCCAG TCGGACTGGA CGGACCACTT TCCGAGATA GGTCTGCTGT AGCGCACCT  
377 V Y T L P P S R E E M T K N Q V S L T C L V K G F Y P S D I A V E

2801 GTGGGAGAGC AATGGGAGC CGGAGAACA CTACAAGAC ACCTCTCCG TCTGTGACTC CGAGGCTCC TTCTCTCT ACAGCAAGT CACGTGGAC  
CACCTCTCG TTACCGCTCG GCCTCTGTT GATGTTCTGG TGCGGAGGC ACAGCTGAG GCTGCCGAGG AGAAGGAGA TGTCTTCTGA GTGGCACCTG  
410 W E S N G Q P E N N Y K T T P P V L D S D G S F F L Y S K L T V D

2901 AAGAGCAGGT GGCAGCAGG GAACTCTTC TATGTCATGA GGTCTGAC AACTACTACA CGCAGAAGAG CCTCTCCCTG TCTCCGGTA  
TTCTCGTCCA CCGTGTGCC CTGTGAGAG AGTAGAGGC ACTACGTACT CCGAGACGTG TTGTGTGATG GGTCTTCTC GGAGAGGAC AGAGGCCAT  
443 K S R W Q Q G N V F S C S V M H E A L H N H Y T Q K S L S L S P G K

3001 AATAAGCATG CGACGGCCCT AGAGTCCCTA ACCTGTGGTT GCGCGGGGC GTTTTATT GTTAACCTAT GTTTGACAGC TTATCATCGA TAAGCTTTAA  
TTATTCGTAC GCTGCCGGA TCTCAGGAT TCGAGCCAA CGCGGGCCCG CAAAAATAA CAATTGAGTA CAACTGTCTG AATAGTAGT ATTGGAATT  
477 O

3101 TCGGTAGTT TATCACAGTT AAATTGCTAA CGCAGTCAGG CACCTGTAT GAAATCTAAC AATCGCTCA TCGTCTCTT CCGCACCGTC ACCCTGGATG  
ACGCCATCAA ATAGTGCTAA TTAAAGATT GCGTCAGTCC GTGGCACATA CTTAGATTG TTACCGAGT AGCAGTAGGA GCCGTGGCAG TGGGACCTAC

3201 CTGTAGGCAT AGCTTGGTT ATGCCGGTAC TGCCGGGCTT CTTGCGGAT ATCGTCCATT CCGACAGCAT CGCCAGTCAC TATGGCGTGC TGCTAGCGT  
GACATCCGTA TCCGAACCAA TAGGCCATG ACGGCCCGA GAACGCCCTA TAGCAGGTAA GGCTGTCTGA GCGTCTAGT ATACCGCAG ACATCGCGA

3301

\*Start Tet Resistance Coding Sequence

Figure 21c

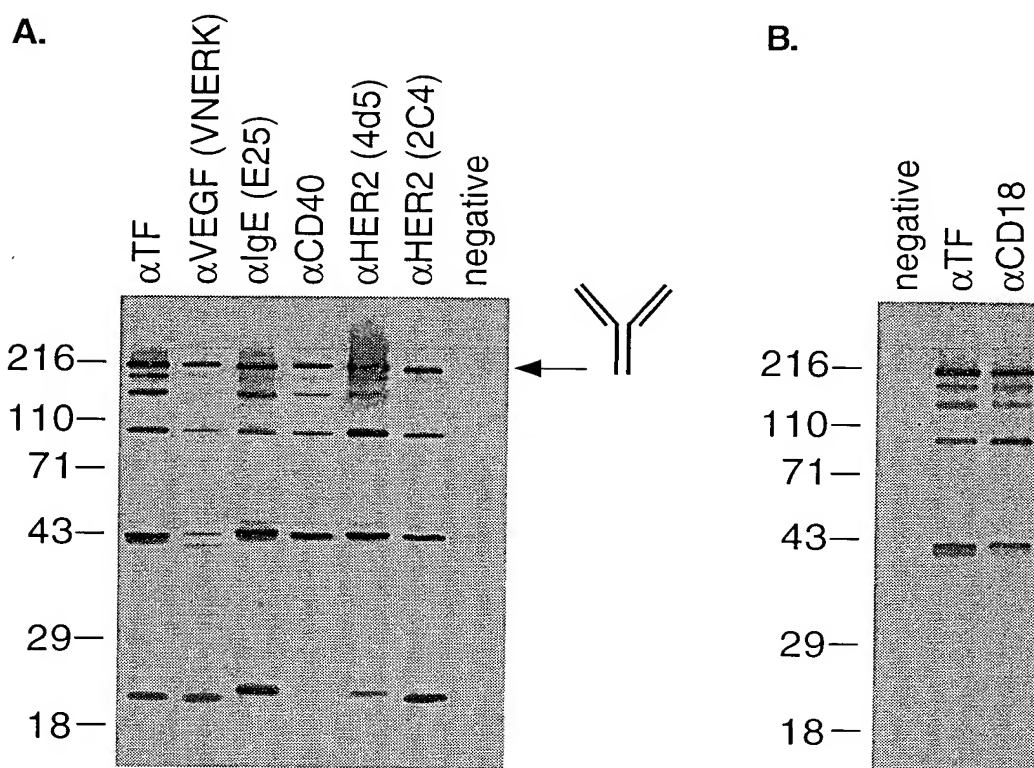


Figure 22